

0590
1/29



OIIPE

RAW SEQUENCE LISTING

DATE: 01/16/2002

PATENT APPLICATION: US/09/903,562A

TIME: 15:58:47

Input Set : N:\Crf3\RULE60\09903562A.raw

Output Set: N:\CRF3\01162002\I903562A.raw

1 <110> APPLICANT: Genentech, Inc.

2 Ashkenazi, Avi

3 Botstein, David

4 Desnoyers, Luc

5 Eaton, Dan L.

6 Ferrara, Napoleone

7 Filvaroff, Ellen

8 Fong, Sherman

9 Gao, Wei-Qiang

10 Gerber, Hanspeter

11 Gerritsen, Mary E.

12 Goddard, A.

13 Godowski, Paul J.

14 Grimaldi, Christopher J.

15 Gurney, Austin L.

16 Hillan, Kenneth, J.

17 Kljavin, Ivar J.

18 Mather, Jennie P.

19 Pan, James

20 Paoni, Nicholas F.

21 Roy, Margaret Ann

22 Stewart, Timothy A.

23 Tumas, Daniel

24 Williams, P. Mickey

25 Wood, William I.

26 <120> TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

27 Acids Encoding the Same

28 <130> FILE REFERENCE: 10466-14

29 <140> CURRENT APPLICATION NUMBER: US/09/903,562A

C--> 30 <141> CURRENT FILING DATE: 2001-07-11

32 <150> PRIOR APPLICATION NUMBER: 09/665,350

33 <151> PRIOR FILING DATE: 2000-09-18

35 <160> NUMBER OF SEQ ID NOS: 423

37 <210> SEQ ID NO: 1

38 <211> LENGTH: 1825

39 <212> TYPE: DNA

40 <213> ORGANISM: Homo Sapien

41 <400> SEQUENCE: 1

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43 cctcgacctc gaccacgcgc tccggggccgg agcagcacgg ccgcaggacc 100

44 tggagctccg gctgcgtctt cccgcagcgc taccgcccat gcgcctgccg 150

45 cgccggggcg cgctgggggct cctgccgctt ctgctgctgc tgccgcccgc 200

46 gccggaggcc gccaaagaagc cgacgccctg ccaccggtgc cgggggctgg 250

ENTERED

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Input Set : N:\Crf3\RULE60\09903562A.raw

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49  cgagattcgc ctgctggaga tcctggaggg gctgtgcgag agcagcgact 400
50  tcgaatgcaa tcagatgcta gaggcgcagg aggagcacct ggaggcctgg 450
51  tggtgcagc tgaagagcga atatcctgac ttattcgagt ggttttgtgt 500
52  gaagacactg aaagtgtgct gctctccagg aacctacggt cccgactgtc 550
53  tcgcatgcca gggcggatcc cagaggccct gcagcgggaa tggccactgc 600
54  agcggagatg ggagcagaca gggcgacggg tcctgccggt gccacatggg 650
55  gtaccagggc ccgctgtgca ctgactgcat ggacggctac ttcagctcgc 700
56  tccggaacga gaccacagc atctgcacag cctgtgacga gtccctgcaag 750
57  acgtgctcgg gcctgaccaa cagagactgc ggcgagtgtg aagtgggctg 800
58  ggtgtctggc gagggcgccct gtgtggatgt ggacgagtgt gcggccgagc 850
59  cgcctccctg cagcgtgcgc cagttctgta agaacgcaa cggctcctac 900
60  acgtgcgaag agtgtgactc cagctgtgtg ggctgcacag gggaaggccc 950
61  aggaaactgt aaagagtgt tctctggcta cgcgaggag cacggacagt 1000
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63  aacgaaaact gctacaatac tccagggagc tacgtctgtg tgtgtcctga 1100
64  cggcttcgaa gaaacggaag atgcctgtgt gccgccggca gaggtgaag 1150
65  ccacagaagg agaaagcccg acacagctgc cctcccgcga agacctgtaa 1200
66  tgtgccggac ttacccttta aattattcag aaggatgtcc cgtggaaaat 1250
67  gtggccctga ggatgccgtc tcctgcagtg gacagcggcg gggagaggct 1300
68  gcctgtcttc taacggttga ttctcatttg tcccttaaac agctgcattt 1350
69  cttggttgtt cttaaacaga cttgtatatt ttgatacagt tctttgtaat 1400
70  aaaattgacc attgtaggta atcaggagga aaaaaaaaaa aaaaaaaaaa 1450
71  aaagggcggc cgcgactcta gagtcgacct gcagaagctt ggccgccatg 1500
72  gcccaacttg tttattgcag cttataatgg ttacaaataa agcaatagca 1550
73  tcacaaatth cacaataaaa gcattttttt cactgcattc tagttgtggt 1600
74  ttgtccaaac tcatcaatgt atcttatcat gtctggatcg ggaattaatt 1650
75  cggcgagcga ccatggcctg aaataacctc tgaaagagga acttggttag 1700
76  gtacctttct aggcggaaag aaccagctgt ggaatgtgtg tcagttaggg 1750
77  tgtggaaagt cccagggctc cccagcaggc agaagtatgc aagcatgcat 1800
78  ctcaattagt cagcaaccca gtttt 1825

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80 <210> SEQ ID NO: 2

81 <211> LENGTH: 353

82 <212> TYPE: PRT

83 <213> ORGANISM: Homo Sapien

84 <400> SEQUENCE: 2

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87  Leu Leu Leu Pro Pro Ala Pro Glu Ala Ala Lys Lys Pro Thr Pro
88      20              25              30
89  Cys His Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met
90      35              40              45
91  Val Asp Thr Ala Lys Lys Asn Phe Gly Gly Asn Thr Ala Trp
92      50              55              60
93  Glu Glu Lys Thr Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu
94      65              70              75
95  Leu Glu Ile Leu Glu Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys
96      80              85              90

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Input Set : N:\Crf3\RULE60\09903562A.raw

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97 Asn Gln Met Leu Glu Ala Gln Glu Glu His Leu Glu Ala Trp Trp
98                               95                               100                               105
99 Leu Gln Leu Lys Ser Glu Tyr Pro Asp Leu Phe Glu Trp Phe Cys
100                               110                               115                               120
101 Val Lys Thr Leu Lys Val Cys Cys Ser Pro Gly Thr Tyr Gly Pro
102                               125                               130                               135
103 Asp Cys Leu Ala Cys Gln Gly Gly Ser Gln Arg Pro Cys Ser Gly
104                               140                               145                               150
105 Asn Gly His Cys Ser Gly Asp Gly Ser Arg Gln Gly Asp Gly Ser
106                               155                               160                               165
107 Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu Cys Thr Asp Cys
108                               170                               175                               180
109 Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr His Ser Ile
110                               185                               190                               195
111 Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly Leu Thr
112                               200                               205                               210
113 Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp Glu
114                               215                               220                               225
115 Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro
116                               230                               235                               240
117 Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr
118                               245                               250                               255
119 Cys Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly
120                               260                               265                               270
121 Pro Gly Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His
122                               275                               280                               285
123 Gly Gln Cys Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr
124                               290                               295                               300
125 Cys Val Arg Lys Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr
126                               305                               310                               315
127 Val Cys Val Cys Pro Asp Gly Phe Glu Glu Thr Glu Asp Ala Cys
128                               320                               325                               330
129 Val Pro Pro Ala Glu Ala Glu Ala Thr Glu Gly Glu Ser Pro Thr
130                               335                               340                               345
131 Gln Leu Pro Ser Arg Glu Asp Leu
132                               350

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134 <210> SEQ ID NO: 3

135 <211> LENGTH: 2206

136 <212> TYPE: DNA

137 <213> ORGANISM: Homo Sapien

138 <400> SEQUENCE: 3

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140 tagagatccc tcgacctcga cccacgcgtc cgccaggccg ggaggcgacg 100
141 cgcccagccg tctaaacggg aacagccctg gctgagggag ctgcagcgca 150
142 gcagagtatc tgacggcgcc aggttgcgta ggtgcggcac gaggagtttt 200
143 cccggcagcg aggaggtcct gagcagcatg gcccggagga gcgccttccc 250
144 tgccgcccgcg ctctggctct ggagcatcct cctgtgcctg ctggcactgc 300
145 gggcgagggc cgggcccgcg caggaggaga gcctgtacct atggatcgat 350
146 gctcaccagg caagagtact cataggattt gaagaagata tcctgattgt 400

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Input Set : N:\Crif3\RULE60\09903562A.raw

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147   ttccagagggg aaaatggcac cttttacaca tgatttcaga aaagcgcaac 450
148   agagaatgcc agctattcct gtcaatatcc attccatgaa ttttacctgg 500
149   caagctgcag ggcaggcaga atacttctat gaattcctgt ccttgcgctc 550
150   cctggataaa ggcacatcag cagatccaac cgtcaatgtc cctctgctgg 600
151   gaacagtgcc tcacaaggca tcagttgttc aagttggttt cccatgtctt 650
152   ggaaaacagg atgggggtgg agcatttgaa gtggatgtga ttgttatgaa 700
153   ttctgaaggc aacaccattc tccaaacacc tcaaaatgct atcttcttta 750
154   aaacatgtca acaagctgag tgcccaggcg ggtgccgaaa tggaggcttt 800
155   tgtaatgaaa gacgcatctg cgagtgtcct gatgggttcc acggacctca 850
156   ctgtgagaaa gccctttgtg cccacgatg tatgaatggg ggactttgtg 900
157   tgactcctgg tttctgcac tgcccacctg gattctatgg agtgaactgt 950
158   gacaaagcaa actgctcaac cacctgcttt aatggaggga cctgtttcta 1000
159   ccctggaaaa tgtatttgcc ctccaggact agaggagag cagtgtgaaa 1050
160   tcagcaaatg cccacaaccc tgcgaaatg gaggtaaatg cattggtaaa 1100
161   agcaaatgtg agtgttccaa aggttaccag ggagacctct gttcaaagcc 1150
162   tgtctgcgag cctggctgtg gtgcacatgg aacctgccat gaaccaaca 1200
163   aatgccaatg tcaagaaggt tggcatggaa gacactgcaa taaaaggtac 1250
164   gaagccagcc tcatacatgc cctgaggcca gcaggcgccc agctcaggca 1300
165   gcacacgcct tcaactaaaa aggccgagga gcggcgggat ccacctgaat 1350
166   ccaattacat ctggtgaact ccgacatctg aaacgtttta agttacacca 1400
167   agttcatagc ctttggttaac ctttcatgtg ttgaatgttc aaataatgtt 1450
168   cattacactt aagaatactg gcctgaattt tattagcttc attataaatc 1500
169   actgagctga tatttactct tccttttaag ttttctaagt acgtctgtag 1550
170   catgatggta tagattttct tgtttcagtg ctttgggaca gattttatat 1600
171   tatgtcaatt gatcagggtt aaattttcag tgtgtagttg gcagatattt 1650
172   tcaaaattac aatgcattta tgggtgtctg gggcagggga acatcagaaa 1700
173   gggttaaattg ggcaaaaatg cgtaagtcac aagaatttgg atggtgcagt 1750
174   taatgttgaa gttacagcat ttcagatttt attgtcagat atttagatgt 1800
175   ttgttacatt tttaaaaatt gctcttaatt tttaaactct caatacaata 1850
176   tattttgacc ttaccattat tccagagatt cagtattaaa aaaaaaaaaa 1900
177   ttacactgtg gtagtggcat ttaacaata taatatattc taaacacaat 1950
178   gaaataggga atataatgta tgaacttttt gcattggctt gaagcaatat 2000
179   aatatattgt aaacaaaaca cagctcttac ctaataaaca ttttatactg 2050
180   tttgtatgta taaaataaag gtgctgcttt agttttttgg aaaaaaaaaa 2100
181   aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gggcgggccg gactctagag 2150
182   tcgacctgca gaagcttggc cgccatggcc caacttgttt attgcagctt 2200

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183 ataagt 2206

185 <210> SEQ ID NO: 4

186 <211> LENGTH: 379

187 <212> TYPE: PRT

188 <213> ORGANISM: Homo Sapien

189 <400> SEQUENCE: 4

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190   Met Ala Arg Arg Ser Ala Phe Pro Ala Ala Ala Leu Trp Leu Trp
191       1             5             10             15
192   Ser Ile Leu Leu Cys Leu Leu Ala Leu Arg Ala Glu Ala Gly Pro
193               20             25             30
194   Pro Gln Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala
195               35             40             45
196   Arg Val Leu Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu

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197		50		55		60
198	Gly Lys Met Ala Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln					
199		65		70		75
200	Arg Met Pro Ala Ile Pro Val Asn Ile His Ser Met Asn Phe Thr					
201		80		85		90
202	Trp Gln Ala Ala Gly Gln Ala Glu Tyr Phe Tyr Glu Phe Leu Ser					
203		95		100		105
204	Leu Arg Ser Leu Asp Lys Gly Ile Met Ala Asp Pro Thr Val Asn					
205		110		115		120
206	Val Pro Leu Leu Gly Thr Val Pro His Lys Ala Ser Val Val Gln					
207		125		130		135
208	Val Gly Phe Pro Cys Leu Gly Lys Gln Asp Gly Val Ala Ala Phe					
209		140		145		150
210	Glu Val Asp Val Ile Val Met Asn Ser Glu Gly Asn Thr Ile Leu					
211		155		160		165
212	Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr Cys Gln Gln Ala					
213		170		175		180
214	Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys Asn Glu Arg					
215		185		190		195
216	Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His Cys Glu					
217		200		205		210
218	Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys Val					
219		215		220		225
220	Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn					
221		230		235		240
222	Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr					
223		245		250		255
224	Cys Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly					
225		260		265		270
226	Glu Gln Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly					
227		275		280		285
228	Gly Lys Cys Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr					
229		290		295		300
230	Gln Gly Asp Leu Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly					
231		305		310		315
232	Ala His Gly Thr Cys His Glu Pro Asn Lys Cys Gln Cys Gln Glu					
233		320		325		330
234	Gly Trp His Gly Arg His Cys Asn Lys Arg Tyr Glu Ala Ser Leu					
235		335		340		345
236	Ile His Ala Leu Arg Pro Ala Gly Ala Gln Leu Arg Gln His Thr					
237		350		355		360
238	Pro Ser Leu Lys Lys Ala Glu Glu Arg Arg Asp Pro Pro Glu Ser					
239		365		370		375
240	Asn Tyr Ile Trp					
242	<210> SEQ ID NO: 5					
243	<211> LENGTH: 45					
244	<212> TYPE: DNA					
245	<213> ORGANISM: Artificial Sequence					
246	<220> FEATURE:					

VERIFICATION SUMMARY

DATE: 01/16/2002

PATENT APPLICATION: US/09/903,562A

TIME: 15:58:48

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L:30 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:383 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13

L:384 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13

L:385 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13

L:386 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13

L:599 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26

L:1361 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50

L:2930 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:113

L:3309 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:131

L:4388 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:174

L:4498 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:175

L:5373 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:206

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